

From: Sent:

Subject:

To:

Slobodyansky, Elizabeth Friday, February 21, 2003 11:28 PM STIC-Biotech/ChemLib

09/590,375

RECEIVED

FEB 24 2003

Please align SEQ ID NO:1 in the above application with SEQ ID NO: 4 in US 6,197,565.

Thank you.

Élizabeth Slobodyansky, PhD

Primary Examiner Art Unit 1652 CM1 10D11 703-306-3222 MAIL BOX 10D01

B. liebeniformis

Technical Info. Specialist

Technical Info. Specialist

Tel: 308-4994

Searcher:	
Phone:	
Location:	
Date Picked Up:	
Date Completed:	
Searcher Prep/Review:	
Clerical:	
Online time:	_

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (w	here applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):_	

7

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, o ,
o o ,
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                                                                                                                         GENALGION Multiple Sequence Alignment Program Release 5.4
                                                           Solution Parameters:
                                                                                        Mon 24 Feb 103 10:49:49-PST
Compress
           Amino Alphabet
Output line length
                                                                                                                                                                                    IntelliGenetics
```

```
AMINO-Res-length DELECTION-weight LEngth-factor Matching-weight NUCLEIC-Res-length
SPread-factor
                                                            Randomization
                                                         h Identity
h 80
l off
l off
l off
         5.00
1.00
```

Clustered order of selected sequences:

```
9.
. US-09-193-068-4
. US-09-590-375-1
    (1-483)
(1-480)
```

"egion Alignment: (listed in Clustered order)

```
US-09-193-
                                                                                                             US-09-590-
                                                                                                                                                US-09-193-
                                                                                                                                                                                                                                     us-09-590-
                                                                                                                                                                                                                                                                       JS-09-193-
                                                                          consensus
                                                                                                                                                                                                  consensus
                                                                                                                                                                                                                                                                                                                                                                                        109-193-
                                                                                                                                                                                                                                                                                                                                                          -590-
                                                                                                                                                                                                                                                                                                                            sensus
184 WeVsnENGNYDYLmyadIDydHPdVaaElKrWGtWyanELqLDGfRLDAvKHIKFSflrDW
                                                                                                                          123 adRorvISGehlikAWThFhFpGRgstYSDFKWhWyHFdGtDWDesrklNrIykFqgkaWd
                                                                                                  123 tnRwqdISGaytIdAWTgFdFsGRnnaYSDFKWrWfHFnGvDWDqryqeNhIfrFantnWn
                                                                                                                                                                                                                                                                                                                                                                           1 anLNGT1MQYfEWympNDGQHWrRLqnDsAyLaehGITavWIPPAYKGtSQADVGYGAYDL
                                                                                                                                                                                                                          --R---ISG---I-AWT-F-F-GR---YSDFKW-W-HF-G-DWD-----N-I--F----W-
                                                                                                                                                                                             YDLGEF-QKGTVRTKYGTK--L--AI-SL-S-DINVYGDVV-NHK-GAD-TE-V-AV-V-P
                                                                                                                                                                                                                                                                                                                     --LNGT-MQY-EW---NDGQHW-RL--D-A-L---GITA-WIPPAYKG-SQADVGYGAYDL
```

us-09-590-

306 nllrgslveaHPmhaVTFVDNHDTQPGeSLESwVadWFKPLAYAtILTREgGYPnVFYGDy 306 klingtvVskhplksvTfVDNHDTQPGqSLEStVqtWfKpLaYAfILTRESGYPqVFYGDm

--L-G--V--HP----VTFVDNHDTQPG-SLES-V--WFKPLAYA-ILTRE-GYP-VFYGD

US-09-193-

US-09-590-US-09-193-

245 VnHvRektgkemftvaEyWqnDlGALEnYLnktNfnhSvFDVPLhYqFhaAStQGGgYDMR

245 VrHqRneadqdlfvVgEYWkdDvGALEfYLdemNwemSlfDVPLnYnFyrASqOGGsYDMR

V-H-R-----F-V-EYW--D-GALE-YL---N---S-FDVPL-Y-F--AS-QGG-YDMR

consensus

us-09-590-

184 WrVdeENGNYDYLlgsnIDfsHPeVqdElKdWGsWftdELdLDGyRLDAiKHIPFwytsDW

W-V--ENGNYDYL----ID--HP-V--E-K-WG-W---EL-LDG-RLDA-KHI-F----DW

consensus

GPGG-K-MYVGRQNAG-TW-D-TGNV-INGWGEFNGGSVS-YV	consensus
US-09-590- 425 msnGPGGsKwMYVGRQNAGqTWtDlTGNngasVtINgdGWGEFftNGGSVSVYVng	US-09-590-
US-09-193- 428 itdGPGGakrmyvGRQNAGeTWhDiTGNTSepvvINseGWGEFhvNGGSVSiyvqr	US-09-193-
YGtkgI-A-KIL-ARYAYG-QHDYFDH-D-VGWTREG-SSNSGLA	consensus
367 YG ipndnIsakKdmIdelLdARqnYAYGtQHDYFDHwDvVGWTREGsSSrpNSGLAti	US-09-590- 367 YG
US-09-193- 367 YGtkgdsgreIpAlKhkIepiLkARkgYAYGaQHDYFDHhDiYGWTREGdSSvaNSGLAal	US-09-193-

Alignment score =

Scoring matrix:

	4
281	9

Sequence Name

1. US-09-590-375-1 Sequence 1, Application US Description

Length Score Score

Sig. Frame 0.00 0

```
Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ខេត្តប៉ូលីប៉ូរ៉ូដូ</u> Fast Pairwise Comparison of Sequences
Reliense 5.4
                                                                                                                                                                                                                                                                                                                          STDEV
The scores below are sorted by initial score. Significance is calculated based on initial score.
                                               Number of residues:
Number of sequences searched:
Number of scores above cutoff:
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o o
o o
o o
o o
                                                                                                                 Times:
                                                                                                                                                   Scores:
                                                                                                                                                                                                 Randomization group
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Number of sequences searched:
1
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Results file us-09-193-068-4.res made by bshears on Mon 24 Feb 103 10:48:42-PST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Results of the initial comparison of US-09-193-068-4 (1-483) with: File : /home/bshears/slob*.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IntelliGenetics
                                                                                                                                                                                                                                                                                                                                       <u>ω</u>_
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276
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0
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                                                                                                                                                                                                                                                                                    PARAMETERS
                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                 K-tuple
Joining penalty
Window size
                                                                                                                                    Median
0
                                                 480
1
1
                                                                                                                                                                                                                                                                                                                                   153
                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                    Standard Deviation 0.00
                                                                                               Total Elapsed 00:00:00:00.00
                                                                                                                                                                                                                                                                                                                                   215
                                                                                                                                                                                                                                                                                                                                   245
                                                                                                                                                                                                                                    20
32
                                                                                                                                                                                                                                                                                                                                  276
```

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

440 450 460 470 480 x GGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR	370 380 390 400 410 420 430 VFYGDMYGTKGDSQREIPALKHKIEPILKARKOYAYGAQHDYFDHHDIYGWTREGDSSYRANSGLAALITDGP	290 300 310 320 340 350 360 HYQFHAASTQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ	220 230 240 250 260 270 280 TWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPL	150 160 170 180 190 200 210 GRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFOGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWG	80 90 100 110 120 130 140; VRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHLIKAWTHFHFP	X 10 20 30 40 50 60 70 ANLIGTLMQYFEWYMPNDGOHWRRLQNDSAYLAEHGITANWIPPAYKGTSOADVGYGAYDLYDLGEFHQKGT	Initial Score = 276 Optimized Score = 301 Significance = 0.00 Residue Identity = 62% Matches = 302 Mismatches = 178 Gaps = 3 Conservative Substitutions = 0	1. US-09-193-068-4 (1-483) US-09-550-375-1 Sequence 1, Application US/09590375 Sequence 1, Application US/09590375 Sequence 1, Application US/09590375 GENERAL INFORMATION: APPLICANT: ENDO, Keiji et al. TITLE OF INVENTION: MUTANT ALPHA-AMYLASES FILE REFERENCE: 2173-0120P CURRENT APPLICATION NUMBER: US/09/590,375 CURRENT FILING DATE: 2000-06-09 PRIOR APPLICATION UMBER: US/09/590,375 CURRENT FILING DATE: 1999-06-10 NUMBER OF SEQ ID NOS: 23 SEQ ID NO 1 LENGTH: 480 TYPE: PRT ORGANISM: Bacillus sp. KSM-K38
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